

## SEQUENCE LISTING

<110> SIMMONS, ANTHONY  
CHEN, JIANMIN

<120> COMPOSITIONS AND METHODS FOR HERPES SIMPLEX PROPHYLAXIS  
AND TREATMENT

<130> UTFG:263WO

<140> UNKNOWN

<141> 2004-07-26

<150> 60/489,984

<151> 2003-07-23

<160> 36

<170> PatentIn Ver. 2.1

<210> 1

<211> 921

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 1

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gacgcggccc agccggccag gcgcgcgcgc cgtacgaagc ttggtaccga gctcggatcc 120
gacatccaga tgacccagtc tccatcctcc ttatctgcct ctctgggaga aagagtcagt 180
ctcacttgctc gggcaagtca ggaaattagt gcttacttaa gctggcttca gcagaaacca 240
gatggaacta ttaaacgcct gatctacgcc gcattccactt tagattctgg tgtcccaaaa 300
aggttcagtg gcagtaggtc tgggtcagat tattctctca ccatcagcag ccttgagtct 360
gaagattttg cagactatta ctgtctacaa tatgctagtt atccgctcac gttcggtgct 420
gggaccaagc tggagctggg cgggtggcga tcgggtggag gaggcagcgg aggcggtggt 480
tcggtgaagc tgcaggagtc tggacctgag ctggtgaagc ctggggcttc agtgaagatg 540
tcctgcaagg cttctggcta caccttcaca agctcctatg tacactgggt gaagcagagg 600
cctggacagg gacttgagtg gattggatgg atttatcctg gacatagtag tactaagtac 660
aatgagaagt tcatgggcaa gaccatattg actgcggaca aatcctccag cacagcctac 720
atgttgctca gcagcctgac ctctgaggac tctgcgatat atttctgtac aaggcaggag 780
gtacgactct ggtacttcga tgtctggggc gcagggacca cggtcaccgt ctccgcggcc 840
gtcagaggag ggcccgaaca aaaactcatc tcagaagagg atctgaatag cgccgtcgac 900
catcatcatc atcatcattg a                                     921

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<210> 2

<211> 306

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Peptide

<400> 2

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Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1             5             10             15
Gly Ser Thr Gly Asp Ala Ala Gln Pro Ala Arg Arg Ala Arg Arg Thr
          20             25             30

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Lys Leu Gly Thr Glu Leu Gly Ser Asp Ile Gln Met Thr Gln Ser Pro  
           35                          40                          45  
 Ser Ser Leu Ser Ala Ser Leu Gly Glu Arg Val Ser Leu Thr Cys Arg  
           50                          55                          60  
 Ala Ser Gln Glu Ile Ser Ala Tyr Leu Ser Trp Leu Gln Gln Lys Pro  
           65                          70                          75                          80  
 Asp Gly Thr Ile Lys Arg Leu Ile Tyr Ala Ala Ser Thr Leu Asp Ser  
                           85                          90                          95  
 Gly Val Pro Lys Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser  
                           100                          105                          110  
 Leu Thr Ile Ser Ser Leu Glu Ser Glu Asp Phe Ala Asp Tyr Tyr Cys  
           115                          120                          125  
 Leu Gln Tyr Ala Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu  
           130                          135                          140  
 Glu Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly  
   145                          150                          155                          160  
 Ser Val Lys Leu Gln Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala  
                           165                          170                          175  
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Ser  
                           180                          185                          190  
 Tyr Val His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile  
           195                          200                          205  
 Gly Trp Ile Tyr Pro Gly His Ser Ser Thr Lys Tyr Asn Glu Lys Phe  
           210                          215                          220  
 Met Gly Lys Thr Ile Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr  
   225                          230                          235                          240  
 Met Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile Tyr Phe Cys  
                           245                          250                          255  
 Thr Arg Gln Glu Val Arg Leu Trp Tyr Phe Asp Val Trp Gly Ala Gly  
           260                          265                          270  
 Thr Thr Val Thr Val Ser Ala Ala Ala Arg Gly Gly Pro Glu Gln Lys  
           275                          280                          285  
 Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His His His His  
           290                          295                          300  
 His His  
 305

&lt;210&gt; 3

&lt;211&gt; 15

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic

## Primer

<400> 3  
tgggtgggaag atggatacag 20

<210> 4  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 4  
ggatgatcg tgatracmca rgatgaactc tc 32

<210> 5  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 5  
ggatgatcw tgmtgaccca awtccactc tc 32

<210> 6  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 6  
ggatgatcg tkctcacyca rtctccagca at 32

<210> 7  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 7  
ctgwtgttct ggattcctg 19

<210> 8  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 8

gtgctctgga ttcgggaa

18

<210> 9

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 9

tcagcttcyt gctaatacagt g

21

<210> 10

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 10

tgggtatctg gtrcstgtg

19

<210> 11

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 11

gtttcmaggt rccagatgt

19

<210> 12

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 12

tgttttcaag gtrccagatg t

21

<210> 13

<211> 20

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
Primer

&lt;400&gt; 13

ctstggttgt ctggtgttga

20

&lt;210&gt; 14

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
Primer

&lt;400&gt; 14

tgctkckctg ggttccag

18

&lt;210&gt; 15

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
Primer

&lt;400&gt; 15

taacccttga ccaggcatcc

20

&lt;210&gt; 16

&lt;211&gt; 36

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
Primer

&lt;400&gt; 16

gaggtgaagc tgcaggagtc aggacctagc ctggtg

36

&lt;210&gt; 17

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
Primer

&lt;400&gt; 17

aggtvmaact gcagvagtcw gg

22

&lt;210&gt; 18

&lt;211&gt; 22

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 18  
aggtvvagct gcagvagtcw gg 22

<210> 19  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 19  
actgcaggtr tccactcc 18

<210> 20  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 20  
rctacaggtg tccactcc 18

<210> 21  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 21  
gcyacagmtg tccactcc 18

<210> 22  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 22  
actgcaggtg tcctctct 18

<210> 23  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 23  
rctrcaggyg tccactct

18

<210> 24  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 24  
ccaagctgtg tcctrtcc

18

<210> 25  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 25  
ccaagctgtg tcctrtcc

18

<210> 26  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 26  
tgttgacagy cvttcckggt

20

<210> 27  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 27  
taytttaaaa rgtgtcmagt gt

22

<210> 28  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 28  
ctyttaaaag gkggtccagwg 20

<210> 29  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 29  
cytttamatg gstatccagtg t 21

<210> 30  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 30  
atggcagcwg cycaaag 17

<210> 31  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 31  
cttttaaaag wtgtccagkg t 21

<210> 32  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer



<400> 32  
cttcctgatg gcagtgggtt

19

<210> 33  
<211> 904  
<212> PRT  
<213> human herpesvirus 1

<400> 33  
Met Arg Gln Gly Ala Pro Ala Arg Gly Arg Arg Trp Phe Val Val Trp  
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20 25 30  
Ser Ser Pro Gly Thr Pro Gly Val Ala Ala Ala Thr Gln Ala Ala Asn  
35 40 45  
Gly Gly Pro Ala Thr Pro Ala Pro Pro Ala Pro Gly Ala Pro Pro Thr  
50 55 60  
Gly Asp Pro Lys Pro Lys Lys Asn Arg Lys Pro Lys Pro Pro Lys Pro  
65 70 75 80  
Pro Arg Pro Ala Gly Asp Asn Ala Thr Val Ala Ala Gly His Ala Thr  
85 90 95  
Leu Arg Glu His Leu Arg Asp Ile Lys Ala Glu Asn Thr Asp Ala Asn  
100 105 110  
Phe Tyr Val Cys Pro Pro Pro Thr Gly Ala Thr Val Val Gln Phe Glu  
115 120 125  
Gln Pro Arg Arg Cys Pro Thr Arg Pro Glu Gly Gln Asn Tyr Thr Glu  
130 135 140  
Gly Ile Ala Val Val Phe Lys Glu Asn Ile Ala Pro Tyr Lys Phe Lys  
145 150 155 160  
Ala Thr Met Tyr Tyr Lys Asp Val Thr Val Ser Gln Val Trp Phe Gly  
165 170 175  
His Arg Tyr Ser Gln Phe Met Gly Ile Phe Glu Asp Arg Ala Pro Val  
180 185 190  
Pro Phe Glu Glu Val Ile Asp Lys Ile Asn Ala Lys Gly Val Cys Arg  
195 200 205  
Ser Thr Ala Lys Tyr Val Arg Asn Asn Leu Glu Thr Thr Ala Phe His  
210 215 220  
Arg Asp Asp His Glu Thr Asp Met Glu Leu Lys Pro Ala Asn Ala Ala  
225 230 235 240  
Thr Arg Thr Ser Arg Gly Trp His Thr Thr Asp Leu Lys Tyr Asn Pro  
245 250 255  
Ser Arg Val Glu Ala Phe His Arg Tyr Gly Thr Thr Val Asn Cys Ile  
260 265 270  
Val Glu Glu Val Asp Ala Arg Ser Val Tyr Pro Tyr Asp Glu Phe Val  
275 280 285

Leu Ala Thr Gly Asp Phe Val Tyr Met Ser Pro Phe Tyr Gly Tyr Arg  
 290 295 300  
 Glu Gly Ser His Thr Glu His Thr Ser Tyr Ala Ala Asp Arg Phe Lys  
 305 310 315 320  
 Gln Val Asp Gly Phe Tyr Ala Arg Asp Leu Thr Thr Lys Ala Arg Ala  
 325 330 335  
 Thr Ala Pro Thr Thr Arg Asn Leu Leu Thr Thr Pro Lys Phe Thr Val  
 340 345 350  
 Ala Trp Asp Trp Val Pro Lys Arg Pro Ser Val Cys Thr Met Thr Lys  
 355 360 365  
 Trp Gln Glu Val Asp Glu Met Leu Arg Ser Glu Tyr Gly Gly Ser Phe  
 370 375 380  
 Arg Phe Ser Ser Asp Ala Ile Ser Thr Thr Phe Thr Thr Asn Leu Thr  
 385 390 395 400  
 Glu Tyr Pro Leu Ser Arg Val Asp Leu Gly Asp Cys Ile Gly Lys Asp  
 405 410 415  
 Ala Arg Asp Ala Met Asp Arg Ile Phe Ala Arg Arg Tyr Asn Ala Thr  
 420 425 430  
 His Ile Lys Val Gly Gln Pro Gln Tyr Tyr Leu Ala Asn Gly Gly Phe  
 435 440 445  
 Leu Ile Ala Tyr Gln Pro Leu Leu Ser Asn Thr Leu Ala Glu Leu Tyr  
 450 455 460  
 Val Arg Glu His Leu Arg Glu Gln Ser Arg Lys Pro Pro Asn Pro Thr  
 465 470 475 480  
 Pro Pro Pro Pro Gly Ala Ser Ala Asn Ala Ser Val Glu Arg Ile Lys  
 485 490 495  
 Thr Thr Ser Ser Ile Glu Phe Ala Arg Leu Gln Phe Thr Tyr Asn His  
 500 505 510  
 Ile Gln Arg His Val Asn Asp Met Leu Gly Arg Val Ala Ile Ala Trp  
 515 520 525  
 Cys Glu Leu Gln Asn His Glu Leu Thr Leu Trp Asn Glu Ala Arg Lys  
 530 535 540  
 Leu Asn Pro Asn Ala Ile Ala Ser Ala Thr Val Gly Arg Arg Val Ser  
 545 550 555 560  
 Ala Arg Met Leu Gly Asp Val Met Ala Val Ser Thr Cys Val Pro Val  
 565 570 575  
 Ala Ala Asp Asn Val Ile Val Gln Asn Ser Met Arg Ile Ser Ser Arg  
 580 585 590  
 Pro Gly Ala Cys Tyr Ser Arg Pro Leu Val Ser Phe Arg Tyr Glu Asp  
 595 600 605  
 Gln Gly Pro Leu Val Glu Gly Gln Leu Gly Glu Asn Asn Glu Leu Arg  
 610 615 620

Leu Thr Arg Asp Ala Ile Glu Pro Cys Thr Val Gly His Arg Arg Tyr  
 625 630 635 640  
 Phe Thr Phe Gly Gly Gly Tyr Val Tyr Phe Glu Glu Tyr Ala Tyr Ser  
 645 650 655  
 His Gln Leu Ser Arg Ala Asp Ile Thr Thr Val Ser Thr Phe Ile Asp  
 660 665 670  
 Leu Asn Ile Thr Met Leu Glu Asp His Glu Phe Val Pro Leu Glu Val  
 675 680 685  
 Tyr Thr Arg His Glu Ile Lys Asp Ser Gly Leu Leu Asp Tyr Thr Glu  
 690 695 700  
 Val Gln Arg Arg Asn Gln Leu His Asp Leu Arg Phe Ala Asp Ile Asp  
 705 710 715 720  
 Thr Val Ile His Ala Asp Ala Asn Ala Ala Met Phe Ala Gly Leu Gly  
 725 730 735  
 Ala Phe Phe Glu Gly Met Gly Asp Leu Gly Arg Ala Val Gly Lys Val  
 740 745 750  
 Val Met Gly Ile Val Gly Gly Val Val Ser Ala Val Ser Gly Val Ser  
 755 760 765  
 Ser Phe Met Ser Asn Pro Phe Gly Ala Leu Ala Val Gly Leu Leu Val  
 770 775 780  
 Leu Ala Gly Leu Ala Ala Ala Phe Phe Ala Phe Arg Tyr Val Met Arg  
 785 790 795 800  
 Leu Gln Ser Asn Pro Met Lys Ala Leu Tyr Pro Leu Thr Thr Lys Glu  
 805 810 815  
 Leu Lys Asn Pro Thr Asn Pro Asp Ala Ser Gly Glu Gly Glu Glu Gly  
 820 825 830  
 Gly Asp Phe Asp Glu Ala Lys Leu Ala Glu Ala Arg Glu Met Ile Arg  
 835 840 845  
 Tyr Met Ala Leu Val Ser Ala Met Glu Arg Thr Glu His Lys Ala Lys  
 850 855 860  
 Lys Lys Gly Thr Ser Ala Leu Leu Ser Ala Lys Val Thr Asp Met Val  
 865 870 875 880  
 Met Arg Lys Arg Arg Asn Thr Asn Tyr Thr Gln Val Pro Asn Lys Asp  
 885 890 895  
 Gly Asp Ala Asp Glu Asp Asp Leu  
 900  
 <210> 34  
 <211> 904  
 <212> PRT  
 <213> human herpesvirus 2  
 <400> 34  
 Met Arg Gly Gly Gly Leu Ile Cys Ala Leu Val Val Gly Ala Leu Val

1	5	10	15
Ala Ala Val Ala Ser Ala Ala Pro Ala Ala Pro Ala Ala Pro Arg Ala	20	25	30
Ser Gly Gly Val Ala Ala Thr Val Ala Ala Asn Gly Gly Pro Ala Ser	35	40	45
Arg Pro Pro Pro Val Pro Ser Pro Ala Thr Thr Lys Ala Arg Lys Arg	50	55	60
Lys Thr Lys Lys Pro Pro Lys Arg Pro Glu Ala Thr Pro Pro Pro Asp	65	70	75
Ala Asn Ala Thr Val Ala Ala Gly His Ala Thr Leu Arg Ala His Leu	85	90	95
Arg Glu Ile Lys Val Glu Asn Ala Asp Ala Gln Phe Tyr Val Cys Pro	100	105	110
Pro Pro Thr Gly Ala Thr Val Val Gln Phe Glu Gln Pro Arg Arg Cys	115	120	125
Pro Thr Arg Pro Glu Gly Gln Asn Tyr Thr Glu Gly Ile Ala Val Val	130	135	140
Phe Lys Glu Asn Ile Ala Pro Tyr Lys Phe Lys Ala Thr Met Tyr Tyr	145	150	155
Lys Asp Val Thr Val Ser Gln Val Trp Phe Gly His Arg Tyr Ser Gln	165	170	175
Phe Met Gly Ile Phe Glu Asp Arg Ala Pro Val Pro Phe Glu Glu Val	180	185	190
Ile Asp Lys Ile Asn Thr Lys Gly Val Cys Arg Ser Thr Ala Lys Tyr	195	200	205
Val Arg Asn Asn Met Glu Thr Thr Ala Phe His Arg Asp Asp His Glu	210	215	220
Thr Asp Met Glu Leu Lys Pro Ala Lys Val Ala Thr Arg Thr Ser Arg	225	230	235
Gly Trp His Thr Thr Asp Leu Lys Tyr Asn Pro Ser Arg Val Glu Ala	245	250	255
Phe His Arg Tyr Gly Thr Thr Val Asn Cys Ile Val Glu Glu Val Asp	260	265	270
Ala Arg Ser Val Tyr Pro Tyr Asp Glu Phe Val Leu Ala Thr Gly Asp	275	280	285
Phe Val Tyr Met Ser Pro Phe Tyr Gly Tyr Arg Glu Gly Ser His Thr	290	295	300
Glu His Thr Ser Tyr Ala Ala Asp Arg Phe Lys Gln Val Asp Gly Phe	305	310	315
Tyr Ala Arg Asp Leu Thr Thr Lys Ala Arg Ala Thr Ser Pro Thr Thr	325	330	335
Arg Asn Leu Leu Thr Thr Pro Lys Phe Thr Val Ala Trp Asp Trp Val			

340	345	350
Pro Lys Arg Pro Ala Val Cys Thr Met Thr Lys Trp Gln Glu Val Asp 355 360 365		
Glu Met Leu Arg Ala Glu Tyr Gly Gly Ser Phe Arg Phe Ser Ser Asp 370 375 380		
Ala Ile Ser Thr Thr Phe Thr Thr Asn Leu Thr Glu Tyr Ser Leu Ser 385 390 395 400		
Arg Val Asp Leu Gly Asp Cys Ile Gly Arg Asp Ala Arg Glu Ala Ile 405 410 415		
Asp Arg Met Phe Ala Arg Lys Tyr Asn Ala Thr His Ile Lys Val Gly 420 425 430		
Gln Pro Gln Tyr Tyr Leu Ala Thr Gly Gly Phe Leu Ile Ala Tyr Gln 435 440 445		
Pro Leu Leu Ser Asn Thr Leu Ala Glu Leu Tyr Val Arg Glu Tyr Met 450 455 460		
Arg Glu Gln Asp Arg Lys Pro Arg Asn Ala Thr Pro Ala Pro Leu Arg 465 470 475 480		
Glu Ala Pro Ser Ala Asn Ala Ser Val Glu Arg Ile Lys Thr Thr Ser 485 490 495		
Ser Ile Glu Phe Ala Arg Leu Gln Phe Thr Tyr Asn His Ile Gln Arg 500 505 510		
His Val Asn Asp Met Leu Gly Arg Ile Ala Val Ala Trp Cys Glu Leu 515 520 525		
Gln Asn His Glu Leu Thr Leu Trp Asn Glu Ala Arg Lys Leu Asn Pro 530 535 540		
Asn Ala Ile Ala Ser Ala Thr Val Gly Arg Arg Val Ser Ala Arg Met 545 550 555 560		
Leu Gly Asp Val Met Ala Val Ser Thr Cys Val Pro Val Ala Pro Asp 565 570 575		
Asn Val Ile Val Gln Asn Ser Met Arg Val Ser Ser Arg Pro Gly Thr 580 585 590		
Cys Tyr Ser Arg Pro Leu Val Ser Phe Arg Tyr Glu Asp Gln Gly Pro 595 600 605		
Leu Ile Glu Gly Gln Leu Gly Glu Asn Asn Glu Leu Arg Leu Thr Arg 610 615 620		
Asp Ala Leu Glu Pro Cys Thr Val Gly His Arg Arg Tyr Phe Ile Phe 625 630 635 640		
Gly Gly Gly Tyr Val Tyr Phe Glu Glu Tyr Ala Tyr Ser His Gln Leu 645 650 655		
Ser Arg Ala Asp Val Thr Thr Val Ser Thr Phe Ile Asp Leu Asn Ile 660 665 670		
Thr Met Leu Glu Asp His Glu Phe Val Pro Leu Glu Val Tyr Thr Arg		

675                                      680                                      685  
 His Glu Ile Lys Asp Ser Gly Leu Leu Asp Tyr Thr Glu Val Gln Arg  
 690                                      695                                      700  
 Arg Asn Gln Leu His Asp Leu Arg Phe Ala Asp Ile Asp Thr Val Ile  
 705                                      710                                      715                                      720  
 Arg Ala Asp Ala Asn Ala Ala Met Phe Ala Gly Leu Cys Ala Phe Phe  
 725                                      730                                      735  
 Glu Gly Met Gly Asp Leu Gly Arg Ala Val Gly Lys Val Val Met Gly  
 740                                      745                                      750  
 Val Val Gly Gly Val Val Ser Ala Val Ser Gly Val Ser Ser Phe Met  
 755                                      760                                      765  
 Ser Asn Pro Phe Gly Ala Leu Ala Val Gly Leu Leu Val Leu Ala Gly  
 770                                      775                                      780  
 Leu Val Ala Ala Phe Phe Ala Phe Arg Tyr Val Leu Gln Leu Gln Arg  
 785                                      790                                      795                                      800  
 Asn Pro Met Lys Ala Leu Tyr Pro Leu Thr Thr Lys Glu Leu Lys Thr  
 805                                      810                                      815  
 Ser Asp Pro Gly Gly Val Gly Gly Glu Gly Glu Glu Gly Ala Glu Gly  
 820                                      825                                      830  
 Gly Gly Phe Asp Glu Ala Lys Leu Ala Glu Ala Arg Glu Met Ile Arg  
 835                                      840                                      845  
 Tyr Met Ala Leu Val Ser Ala Met Glu Arg Thr Glu His Lys Ala Arg  
 850                                      855                                      860  
 Lys Lys Gly Thr Ser Ala Leu Leu Ser Ser Lys Val Thr Asn Met Val  
 865                                      870                                      875                                      880  
 Leu Arg Lys Arg Asn Lys Ala Arg Tyr Ser Pro Leu His Asn Glu Asp  
 885                                      890                                      895  
 Glu Ala Gly Asp Glu Asp Glu Leu  
 900

&lt;210&gt; 35

&lt;211&gt; 394

&lt;212&gt; PRT

&lt;213&gt; human herpesvirus 1

&lt;400&gt; 35

Met Gly Gly Ala Ala Ala Arg Leu Gly Ala Val Ile Leu Phe Val Val  
 1                                      5                                      10                                      15

Ile Val Gly Leu His Gly Val Arg Ser Lys Tyr Ala Leu Val Asp Ala  
 20                                      25                                      30

Ser Leu Lys Met Ala Asp Pro Asn Arg Phe Arg Gly Lys Asp Leu Pro  
 35                                      40                                      45

Val Leu Asp Gln Leu Thr Asp Pro Pro Gly Val Arg Arg Val Tyr His  
 50                                      55                                      60

Ile Gln Ala Gly Leu Pro Asp Pro Phe Gln Pro Pro Ser Leu Pro Ile  
 65 70 75 80  
 Thr Val Tyr Tyr Ala Val Leu Glu Arg Ala Cys Arg Ser Val Leu Leu  
 85 90 95  
 Asn Ala Pro Ser Glu Ala Pro Gln Ile Val Arg Gly Ala Ser Glu Asp  
 100 105 110  
 Val Arg Lys Gln Pro Tyr Asn Leu Thr Ile Ala Trp Phe Arg Met Gly  
 115 120 125  
 Gly Asn Cys Ala Ile Pro Ile Thr Val Met Glu Tyr Thr Glu Cys Ser  
 130 135 140  
 Tyr Asn Lys Ser Leu Gly Ala Cys Pro Ile Arg Thr Gln Pro Arg Trp  
 145 150 155 160  
 Asn Tyr Tyr Asp Ser Phe Ser Ala Val Ser Glu Asp Asn Leu Gly Phe  
 165 170 175  
 Leu Met His Ala Pro Ala Phe Glu Thr Ala Gly Thr Tyr Leu Arg Leu  
 180 185 190  
 Val Lys Ile Asn Asp Trp Thr Glu Ile Thr Gln Phe Ile Leu Glu His  
 195 200 205  
 Arg Ala Lys Gly Ser Cys Lys Tyr Ala Leu Pro Leu Arg Ile Pro Pro  
 210 215 220  
 Ser Ala Cys Leu Ser Pro Gln Ala Tyr Gln Gln Gly Val Thr Val Asp  
 225 230 235 240  
 Ser Ile Gly Met Leu Pro Arg Phe Ile Pro Glu Asn Gln Arg Thr Val  
 245 250 255  
 Ala Val Tyr Ser Leu Lys Ile Ala Gly Trp His Gly Pro Lys Ala Pro  
 260 265 270  
 Tyr Thr Ser Thr Leu Leu Pro Pro Glu Leu Ser Glu Thr Pro Asn Ala  
 275 280 285  
 Thr Gln Pro Glu Leu Ala Pro Glu Asp Pro Glu Asp Ser Ala Leu Leu  
 290 295 300  
 Glu Asp Pro Val Gly Thr Val Ala Pro Gln Ile Pro Pro Asn Trp His  
 305 310 315 320  
 Ile Pro Ser Ile Gln Asp Ala Ala Thr Pro Tyr His Pro Pro Ala Thr  
 325 330 335  
 Pro Asn Asn Met Gly Leu Ile Ala Gly Ala Val Gly Gly Ser Leu Leu  
 340 345 350  
 Ala Ala Leu Val Ile Cys Gly Ile Val Tyr Trp Met Arg Arg His Thr  
 355 360 365  
 Gln Lys Ala Pro Lys Arg Ile Arg Leu Pro His Ile Arg Glu Asp Asp  
 370 375 380  
 Gln Pro Ser Ser His Gln Pro Leu Phe Tyr  
 385 390

&lt;210&gt; 36

&lt;211&gt; 393

&lt;212&gt; PRT

&lt;213&gt; human herpesvirus 2

&lt;400&gt; 36

Met Gly Arg Leu Thr Ser Gly Val Gly Thr Ala Ala Leu Leu Val Val  
 1 5 10 15

Ala Val Gly Leu Arg Val Val Cys Ala Lys Tyr Ala Leu Ala Asp Pro  
 20 25 30

Ser Leu Lys Met Ala Asp Pro Asn Arg Phe Arg Gly Lys Asn Leu Pro  
 35 40 45

Val Leu Asp Gln Leu Thr Asp Pro Pro Gly Val Lys Arg Val Tyr His  
 50 55 60

Ile Gln Pro Ser Leu Glu Asp Pro Phe Gln Pro Pro Ser Ile Pro Ile  
 65 70 75 80

Thr Val Tyr Tyr Ala Val Leu Glu Arg Ala Cys Arg Ser Val Leu Leu  
 85 90 95

His Ala Pro Ser Glu Ala Pro Gln Ile Val Arg Gly Ala Ser Asp Glu  
 100 105 110

Ala Arg Lys His Thr Tyr Asn Leu Thr Ile Ala Trp Tyr Arg Met Gly  
 115 120 125

Asp Asn Cys Ala Ile Pro Ile Thr Val Met Glu Tyr Thr Glu Cys Pro  
 130 135 140

Tyr Asn Lys Ser Leu Gly Val Cys Pro Ile Arg Thr Gln Pro Arg Trp  
 145 150 155 160

Ser Tyr Tyr Asp Ser Phe Ser Ala Val Ser Glu Asp Asn Leu Gly Phe  
 165 170 175

Leu Met His Ala Pro Ala Phe Glu Thr Ala Gly Thr Tyr Leu Arg Leu  
 180 185 190

Val Lys Ile Asn Asp Trp Thr Glu Ile Thr Gln Phe Ile Leu Glu His  
 195 200 205

Arg Ala Arg Ala Ser Cys Lys Tyr Ala Leu Pro Leu Arg Ile Pro Pro  
 210 215 220

Ala Ala Cys Leu Thr Ser Lys Ala Tyr Gln Gln Gly Val Thr Val Asp  
 225 230 235 240

Ser Ile Gly Met Leu Pro Arg Phe Ile Pro Glu Asn Gln Arg Thr Val  
 245 250 255

Ala Leu Tyr Ser Leu Lys Ile Ala Gly Trp His Gly Pro Lys Pro Pro  
 260 265 270

Tyr Thr Ser Thr Leu Leu Pro Pro Glu Leu Ser Asp Thr Thr Asn Ala  
 275 280 285

Thr Gln Pro Glu Leu Val Pro Glu Asp Pro Glu Asp Ser Ala Leu Leu  
 290 295 300



Glu Asp Pro Ala Gly Thr Val Ser Ser Gln Ile Pro Pro Asn Trp His  
305 310 315 320

Ile Pro Ser Ile Gln Asp Val Ala Pro His His Ala Pro Ala Ala Pro  
325 330 335

Ser Asn Pro Gly Leu Ile Ile Gly Ala Leu Ala Gly Ser Thr Leu Ala  
340 345 350

Val Leu Val Ile Gly Gly Ile Ala Phe Trp Val Arg Arg Arg Ala Gln  
355 360 365

Met Ala Pro Lys Arg Leu Arg Leu Pro His Ile Arg Asp Asp Asp Ala  
370 375 380

Pro Pro Ser His Gln Pro Leu Phe Tyr  
385 390